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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gray, Patrick W.
Schweickart, Vicky L.
Raport, Carol J.
- (ii) TITLE OF INVENTION: Chemokine Receptor Materials and Methods
- (iii) NUMBER OF SEQUENCES: 20
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 - (B) STREET: 6300 Sears Tower, 233 S. Wacker Drive
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: USA
 - (F) ZIP: 60606
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Noland, Greta E.
 - (B) REGISTRATION NUMBER: 35,302
 - (C) REFERENCE/DOCKET NUMBER: 27866/33670
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 312-474-6300
 - (B) TELEFAX: 312-474-0448

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 55..1110
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (D) OTHER INFORMATION: /= "88C polynucleotide and amino acid sequences"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGAAGAGCTG AGACATCCGT TCCCCTACAA GAAACTCTCC CCGGGTGGAA CAAG ATG
Met

1

GAT	TAT	CAA	GTG	TCA	AGT	CCA	ATC	TAT	GAC	ATC	AAT	TAT	TAT	ACA	TCG	105
Asp	Tyr	Gln	Val	Ser	Ser	Pro	Ile	Tyr	Asp	Ile	Asn	Tyr	Tyr	Thr	Ser	
			5					10					15			
GAG	CCC	TGC	CAA	AAA	ATC	AAT	GTG	AAG	CAA	ATC	GCA	GCC	CGC	CTC	CTG	153
Glu	Pro	Cys	Gln	Lys	Ile	Asn	Val	Lys	Gln	Ile	Ala	Ala	Arg	Leu	Leu	
		20					25				30					
CCT	CCG	CTC	TAC	TCA	CTG	GTG	TTC	ATC	TTT	GGT	TTT	GTG	GGC	AAC	ATG	201
Pro	Pro	Leu	Tyr	Ser	Leu	Val	Phe	Ile	Phe	Gly	Phe	Val	Gly	Asn	Met	
	35					40				45						
CTG	GTC	ATC	CTC	ATC	CTG	ATA	AAC	TGC	AAA	AGG	CTG	AAG	AGC	ATG	ACT	249
Leu	Val	Ile	Leu	Ile	Leu	Ile	Asn	Cys	Lys	Arg	Leu	Lys	Ser	Met	Thr	
	50				55				60						65	
GAC	ATC	TAC	CTG	CTC	AAC	CTG	GCC	ATC	TCT	GAC	CTG	TTT	TTC	CTT	CTT	297
Asp	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Leu	Phe	Phe	Leu	Leu	
				70					75					80		
ACT	GTC	CCC	TTC	TGG	GCT	CAC	TAT	GCT	GCC	GCC	CAG	TGG	GAC	TTT	GGA	345
Thr	Val	Pro	Phe	Trp	Ala	His	Tyr	Ala	Ala	Ala	Gln	Trp	Asp	Phe	Gly	
			85					90					95			
AAT	ACA	ATG	TGT	CAA	CTC	TTG	ACA	GGG	CTC	TAT	TTT	ATA	GGC	TTC	TTC	393
Asn	Thr	Met	Cys	Gln	Leu	Leu	Thr	Gly	Leu	Tyr	Phe	Ile	Gly	Phe	Phe	
		100					105					110				
TCT	GGA	ATC	TTC	TTC	ATC	ATC	CTC	CTG	ACA	ATC	GAT	AGG	TAC	CTG	GCT	441
Ser	Gly	Ile	Phe	Phe	Ile	Ile	Leu	Leu	Thr	Ile	Asp	Arg	Tyr	Leu	Ala	
	115					120					125					
GTC	GTC	CAT	GCT	GTG	TTT	GCT	TTA	AAA	GCC	AGG	ACG	GTC	ACC	TTT	GGG	489
Val	Val	His	Ala	Val	Phe	Ala	Leu	Lys	Ala	Arg	Thr	Val	Thr	Phe	Gly	
	130				135				140						145	
GTG	GTG	ACA	AGT	GTG	ATC	ACT	TGG	GTG	GTG	GCT	GTG	TTT	GCG	TCT	CTC	537
Val	Val	Thr	Ser	Val	Ile	Thr	Trp	Val	Val	Ala	Val	Phe	Ala	Ser	Leu	
				150				155						160		
CCA	GGA	ATC	ATC	TTT	ACC	AGA	TCT	CAA	AAA	GAA	GGT	CTT	CAT	TAC	ACC	585
Pro	Gly	Ile	Ile	Phe	Thr	Arg	Ser	Gln	Lys	Glu	Gly	Leu	His	Tyr	Thr	
			165					170					175			
TGC	AGC	TCT	CAT	TTT	CCA	TAC	AGT	CAG	TAT	CAA	TTC	TGG	AAG	AAT	TTC	633
Cys	Ser	Ser	His	Phe	Pro	Tyr	Ser	Gln	Tyr	Gln	Phe	Trp	Lys	Asn	Phe	
		180					185					190				
CAG	ACA	TTA	AAG	ATA	GTC	ATC	TTG	GGG	CTG	GTC	CTG	CCG	CTG	CTT	GTC	681
Gln	Thr	Leu	Lys	Ile	Val	Ile	Leu	Gly	Leu	Val	Leu	Pro	Leu	Leu	Val	
	195					200					205					
ATG	GTC	ATC	TGC	TAC	TCG	GGA	ATC	CTA	AAA	ACT	CTG	CTT	CGG	TGT	CGA	729
Met	Val	Ile	Cys	Tyr	Ser	Gly	Ile	Leu	Lys	Thr	Leu	Leu	Arg	Cys	Arg	
					215					220					225	
AAT	GAG	AAG	AAG	AGG	CAC	AGG	GCT	GTG	AGG	CTT	ATC	TTC	ACC	ATC	ATG	777
Asn	Glu	Lys	Lys	Arg	His	Arg	Ala	Val	Arg	Leu	Ile	Phe	Thr	Ile	Met	
				230					235					240		
ATT	GTT	TAT	TTT	CTC	TTC	TGG	GCT	CCC	TAC	AAC	ATT	GTC	CTT	CTC	CTG	825
Ile	Val	Tyr	Phe	Leu	Phe	Trp	Ala	Pro	Tyr	Asn	Ile	Val	Leu	Leu	Leu	
			245					250					255			
AAC	ACC	TTC	CAG	GAA	TTC	TTT	GGC	CTG	AAT	AAT	TGC	AGT	AGC	TCT	AAC	873
Asn	Thr	Phe	Gln	Glu	Phe	Phe	Gly	Leu	Asn	Asn	Cys	Ser	Ser	Ser	Asn	
		260					265					270				

AGG	TTG	GAC	CAA	GCT	ATG	CAG	GTG	ACA	GAG	ACT	CTT	GGG	ATG	ACG	CAC	921
Arg	Leu	Asp	Gln	Ala	Met	Gln	Val	Thr	Glu	Thr	Leu	Gly	Met	Thr	His	
	275						280					285				
TGC	TGC	ATC	AAC	CCC	ATC	ATC	TAT	GCC	TTT	GTC	GGG	GAG	AAG	TTC	AGA	969
Cys	Cys	Ile	Asn	Pro	Ile	Ile	Tyr	Ala	Phe	Val	Gly	Glu	Lys	Phe	Arg	
	290				295					300					305	
AAC	TAC	CTC	TTA	GTC	TTC	TTC	CAA	AAG	CAC	ATT	GCC	AAA	CGC	TTC	TGC	1017
Asn	Tyr	Leu	Leu	Val	Phe	Phe	Gln	Lys	His	Ile	Ala	Lys	Arg	Phe	Cys	
				310					315					320		
AAA	TGC	TGT	TCT	ATT	TTC	CAG	CAA	GAG	GCT	CCC	GAG	CGA	GCA	AGC	TCA	1065
Lys	Cys	Cys	Ser	Ile	Phe	Gln	Gln	Glu	Ala	Pro	Glu	Arg	Ala	Ser	Ser	
			325					330					335			
GTT	TAC	ACC	CGA	TCC	ACT	GGG	GAG	CAG	GAA	ATA	TCT	GTG	GGC	TTG		1110
Val	Tyr	Thr	Arg	Ser	Thr	Gly	Glu	Gln	Glu	Ile	Ser	Val	Gly	Leu		
			340				345					350				
TGACACGGAC	TCAAGTGGGC	TGGTGACCCA	GTCAGAGTTG	TGCACATGGC	TTAGTTTTCA											1170
TACACAGCCT	GGGCTGGGGG	TGGGGTGGGA	GAGGTCTTTT	TTAAAGGAA	GTTACTGTTA											1230
TAGAGGGTCT	AAGATTCATC	CATTTATTTG	GCATCTGTTT	AAAGTAGATT	AGATCTTTTA											1290
AGCCCATCAA	TTATAGAAAG	CCAAATCAAA	ATATGTTGAT	GAAAAATAGC	AACCTTTTTA											1350
TCTCCCCCTC	ACATGCATCA	AGTTATTGAC	AAACTCTCCC	TTCACTCCGA	AAGTTCCTTA											1410
TGTATATTTA	AAAGAAAGCC	TCAGAGAATT	GCTGATTCTT	GAGTTTAGTG	ATCTGAACAG											1470
AAATACCAAA	ATTATTTTCAG	AAATGTACAA	CTTTTTTACCT	AGTACAAGGC	AACATATAGG											1530
TTGTAAATGT	GTTTAAACA	GGTCTTTGTC	TTGCTATGGG	GAGAAAAGAC	ATGAATATGA											1590
TTAGTAAAGA	AATGACACTT	TTCATGTGTG	ATTTCCCCTC	CAAGGTATGG	TTAATAAGTT											1650
TCACTGACTT	AGAACCAGGC	GAGAGACTTG	TGGCCTGGGA	GAGCTGGGGA	AGCTTCTTAA											1710
ATGAGAAGGA	ATTTGAGTTG	GATCATCTAT	TGCTGGCAAA	GACAGAAGCC	TCACTGCAAG											1770
CACTGCATGG	GCAAGCTTGG	CTGTAGAAGG	AGACAGAGCT	GGTTGGGAAG	ACATGGGGAG											1830
GAAGGACAAG	GCTAGATCAT	GAAGAACCTT	GACGGCATTG	CTCCGTCTAA	GTCATGAGCT											1890
GAGCAGGGAG	ATCCTGGTTG	GTGTTGCAGA	AGGTTTACTC	TGTGGCCAAA	GGAGGGTCAG											1950
GAAGGATGAG	CATTTAGGGC	AAGGAGACCA	CCAACAGCCC	TCAGGTCAGG	GTGAGGATGG											2010
CCTCTGCTAA	GCTCAAGGCG	TGAGGATGGG	AAGGAGGGAG	GTATTCGTAA	GGATGGGAAG											2070
GAGGGAGGTA	TTCGTGCAGC	ATATGAGGAT	GCAGAGTCAG	CAGAACTGGG	GTGGATTGGG											2130
TTTGGAAGTG	AGGGTCAGAG	AGGAGTCAGA	GAGAATCCCT	AGTCTTCAAG	CAGATTGGAG											2190
AAACCCTTGA	AAAGACATCA	AGCACAGAAG	GAGGAGGAGG	AGGTTTAGGT	CAAGAAGAAG											2250
ATGGATTGGT	GTAAAAGGAT	GGGTCTGGTT	TGCAGAGCTT	GAACACAGTC	TCACCCAGAC											2310
TCCAGGCTGT	CTTTCACCTGA	ATGCTTCTGA	CTTCATAGAT	TTCCTTCCCA	TCCCAGCTGA											2370
AATACTGAGG	GGTCTCCAGG	AGGAGACTAG	ATTTATGAAT	ACACGAGGTA	TGAGGTCTAG											

TTCAATAAGC ATCAAACCTCT TAGTTACTCA TTCAGGGATA GCACTGAGCA AAGCATTGAG 2610
CAAAGGGGTC CCATATAGGT GAGGGAAGCC TGAAAACTA AGATGCTGCC TGCCCAGTGC 2670
ACACAAGTGT AGGTATCATT TTCTGCATTT AACCGTCAAT AGGCAAAGGG GGGAAAGGGAC 2730
ATATTCATTT GGAAATAAGC TGCCTTGAGC CTTAAACCC ACAAAAGTAC AATTTACCAG 2790
CCTCCGTATT TCAGACTGAA TGGGGGTGGG GGGGGCGCCT TAGGTACTTA TTCCAGATGC 2850
CTTCTCCAGA CAAACCAGAA GCAACAGAAA AAATCGTCTC TCCCTCCCTT TGAAATGAAT 2910
ATACCCCTTA GTGTTTGGGT ATATTCATTT CAAAGGGAGA GAGAGAGGTT TTTTCTGT 2970
CTTTCTCATA TGATTGTGCA CATACTTGAG ACTGTTTTGA ATTTGGGGGA TGGCTAAAAC 3030
CATCATAGTA CAGGTAAGGT GAGGGAATAG TAAGTGGTGA GAACTACTCA GGAATGAAG 3090
GTGTCAGAAT AATAAGAGGT GCTACTGACT TTCTCAGCCT CTGAATATGA ACGGTGAGCA 3150
TTGTGGCTGT CAGCAGGAAG CAACGAAGGG AAATGTCTTT CCTTTTGCTC TTAAGTTGTG 3210
GAGAGTGCAA CAGTAGCATA GGACCCTACC CTCTGGGCCA AGTCAAAGAC ATTCTGACAT 3270
CTTAGTATTT GCATATTCTT ATGTATGTGA AAGTTACAAA TTGCTTGAAA GAAAATATGC 3330
ATCTAATAAA AAACACCTTC TAAATAAAA AAAAAAAAAA AAAAAAAAAA AAA 3383

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: /= "88C amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
1 5 10 15
Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
20 25 30
Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
35 40 45
Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
50 55 60
Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
65 70 75 80
Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
85 90 95
Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
100 105 110
Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
115 120 125

Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
130 135 140

Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
145 150 155 160

Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
165 170 175

Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
180 185 190

Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
195 200 205

Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
210 215 220

Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
225 230 235 240

Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
245 250 255

Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
260 265 270

Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
275 280 285

His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
290 295 300

Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
305 310 315 320

Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
325 330 335

Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
340 345 350

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 362..1426

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (D) OTHER INFORMATION: /= "88-2B polynucleotide and amino acid sequences"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATAATAATGA TTATTATATT GTTATCATTA TCTAGCCTGT TTTTTCCTGT TTTGTATTTT 60

TTCCTTTTAAA TGCTTTTCAGA AATCTGTATC CCCATTCTTC ACCACCACCC CACAACATTT 120

CTGCTTCTTT	TCCCATGCCG	GGTCATGCTA	ACTTTGAAAG	CTTCAGCTCT	TTCCTTCCTC		180
AATCCTTTTC	CTGGCACCTC	TGATATGCCT	TTTGAAATTC	ATGTTAAAGA	ATCCCTAGGC		240
TGCTATCACA	TGTGGCATCT	TTGTTGAGTA	CATGAATAAA	TCAACTGGTG	TGTTTTACGA		300
AGGATGATTA	TGCTTCATTG	TGGGATTGTA	TTTTTCTTCT	TCTATCACAG	GGAGAAGTGA		360
A ATG ACA ACC TCA CTA GAT ACA GTT GAG ACC TTT GGT ACC ACA TCC							406
Met Thr Thr Ser Leu Asp Thr Val Glu Thr Phe Gly Thr Thr Ser							
1	5	10	15				
TAC TAT GAT GAC GTG GGC CTG CTC TGT GAA AAA GCT GAT ACC AGA GCA							454
Tyr Tyr Asp Asp Val Gly Leu Leu Cys Glu Lys Ala Asp Thr Arg Ala							
20	25	30					
CTG ATG GCC CAG TTT GTG CCC CCG CTG TAC TCC CTG GTG TTC ACT GTG							502
Leu Met Ala Gln Phe Val Pro Pro Leu Tyr Ser Leu Val Phe Thr Val							
35	40	45					
GGC CTC TTG GGC AAT GTG GTG GTG GTG ATG ATC CTC ATA AAA TAC AGG							550
Gly Leu Leu Gly Asn Val Val Val Met Ile Leu Ile Lys Tyr Arg							
50	55	60					
AGG CTC CGA ATT ATG ACC AAC ATC TAC CTG CTC AAC CTG GCC ATT TCG							598
Arg Leu Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser							
65	70	75					
GAC CTG CTC TTC CTC GTC ACC CTT CCA TTC TGG ATC CAC TAT GTC AGG							646
Asp Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg							
80	85	90					
GGG CAT AAC TGG GTT TTT GGC CAT GGC ATG TGT AAG CTC CTC TCA GGG							694
Gly His Asn Trp Val Phe Gly His Gly Met Cys Lys Leu Leu Ser Gly							
100	105	110					
TTT TAT CAC ACA GGC TTG TAC AGC GAG ATC TTT TTC ATA ATC CTG CTG							742
Phe Tyr His Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu							
115	120	125					
ACA ATC GAC AGG TAC CTG GCC ATT GTC CAT GCT GTG TTT GCC CTT CGA							790
Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg							
130	135	140					
GCC CGG ACT GTC ACT TTT GGT GTC ATC ACC AGC ATC GTC ACC TGG GGC							838
Ala Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Val Thr Trp Gly							
145	150	155					
CTG GCA GTG CTA GCA GCT CTT CCT GAA TTT ATC TTC TAT GAG ACT GAA							886
Leu Ala Val Leu Ala Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu							
160	165	170					
GAG TTG TTT GAA GAG ACT CTT TGC AGT GCT CTT TAC CCA GAG GAT ACA							934
Glu Leu Phe Glu Glu Thr Leu Cys Ser Ala Leu Tyr Pro Glu Asp Thr							
180	185	190					
GTA TAT AGC TGG AGG CAT TTC CAC ACT CTG AGA ATG ACC ATC TTC TGT							982
Val Tyr Ser Trp Arg His Phe His Thr Leu Arg Met Thr Ile Phe Cys							
195	200	205					
CTC GTT CTC CCT CTG CTC GTT ATG GCC ATC TGC TAC ACA GGA ATC ATC							1030
Leu Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile							
210	215	220					
AAA ACG CTG CTG AGG TGC CCC AGT AAA AAA AAG TAC AAG GCC ATC CGG							1078
Lys Thr Leu Leu Arg Cys Pro Ser Lys Lys Lys Tyr Lys Ala Ile Arg							
225	230	235					

CTC	ATT	TTT	GTC	ATC	ATG	GCG	GTG	TTT	TTC	ATT	TTC	TGG	ACA	CCC	TAC	1126
Leu	Ile	Phe	Val	Ile	Met	Ala	Val	Phe	Phe	Ile	Phe	Trp	Thr	Pro	Tyr	
240					245					250					255	
AAT	GTG	GCT	ATC	CTT	CTC	TCT	TCC	TAT	CAA	TCC	ATC	TTA	TTT	GGA	AAT	1174
Asn	Val	Ala	Ile	Leu	Leu	Ser	Ser	Tyr	Gln	Ser	Ile	Leu	Phe	Gly	Asn	
				260					265					270		
GAC	TGT	GAG	CGG	AGC	AAG	CAT	CTG	GAC	CTG	GTC	ATG	CTG	GTG	ACA	GAG	1222
Asp	Cys	Glu	Arg	Ser	Lys	His	Leu	Asp	Leu	Val	Met	Leu	Val	Thr	Glu	
			275					280					285			
GTG	ATC	GCC	TAC	TCC	CAC	TGC	TGC	ATG	AAC	CCG	GTG	ATC	TAC	GCC	TTT	1270
Val	Ile	Ala	Tyr	Ser	His	Cys	Cys	Met	Asn	Pro	Val	Ile	Tyr	Ala	Phe	
		290					295					300				
GTT	GGA	GAG	AGG	TTC	CGG	AAG	TAC	CTG	CGC	CAC	TTC	TTC	CAC	AGG	CAC	1318
Val	Gly	Glu	Arg	Phe	Arg	Lys	Tyr	Leu	Arg	His	Phe	Phe	His	Arg	His	
	305					310					315					
TTG	CTC	ATG	CAC	CTG	GGC	AGA	TAC	ATC	CCA	TTC	CTT	CCT	AGT	GAG	AAG	1366
Leu	Leu	Met	His	Leu	Gly	Arg	Tyr	Ile	Pro	Phe	Leu	Pro	Ser	Glu	Lys	
320					325				330						335	
CTG	GAA	AGA	ACC	AGC	TCT	GTC	TCT	CCA	TCC	ACA	GCA	GAG	CCG	GAA	CTC	1414
Leu	Glu	Arg	Thr	Ser	Ser	Val	Ser	Pro	Ser	Thr	Ala	Glu	Pro	Glu	Leu	
				340					345					350		
TCT	ATT	GTG	TTT	TAGGTCAGAT	GCAGAAAATT	GCCTAAAGAG	GAAGGACCAA									1466
Ser	Ile	Val	Phe													
			355													
GGAGATGAAG	CAAACACATT	AAGCCTTCCA	CACTCACCTC	TAAAACAGTC	CTTCAAACCTT											1526
CCAGTGCAAC	ACTGAAGCTC	TTGAAGACAC	TGAAATATAC	ACACAGCAGT	AGCAGTAGAT											1586
GCGATGTACCC	TAAGGTCATT	ACCACAGGCC	AGGGGCTGGG	CAGCGTACTC	ATCATCAACC											1646
CTAAAAAGCA	GAGCTTTGCT	TCTCTCTCTA	AAATGAGTTA	CCTACATTTT	AATGCACCTG											1706
AATGTTAGAT	AGTTACTATA	TGCCGCTACA	AAAAGGTAAA	ACTTTTTTATA	TTTTTATACAT											1766
TAACTTCAGC	CAGCTATTGA	TATAAATAAA	ACATTTTTCAC	ACAATACAAT	AAGTTAACTA											1826
TTTTATTTTC	TAATGTGCCT	AGTTCTTTCC	CTGCTTAATG	AAAAGCTTGT	TTTTTCAGTG											1886
TGAATAAATA	ATCGTAAGCA	ACAAAAAAA														1915

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (D) OTHER INFORMATION: /= "88-2B amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Thr	Thr	Ser	Leu	Asp	Thr	Val	Glu	Thr	Phe	Gly	Thr	Thr	Ser	Tyr
1				5				10						15	

1

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (D) OTHER INFORMATION: /= "V28degf2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACGGATCCA TYGAYAGRTA CCTGGCYATY GTCC

34

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (D) OTHER INFORMATION: /= "V28degr2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCTAAGCTTT TRTAGGGDGT CCAYAAGAGY AA

32

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (D) OTHER INFORMATION: /= "88c-r4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATAAGCCTC ACAGCCCTGT G

21

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (D) OTHER INFORMATION: /= "88c-rlb"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCTAAGCTTG ATGACTATCT TTAATGTC

28

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: /= "88-2B-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCCTCTAGAC TAAACACAA TAGAGAG

27

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: /= "88-2B-5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCTAAGCTTA TCACAGGGAG AAGTGAAATG

30

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: /= "88-2B-f1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGTGCTAGCA GCTCTTCCTG

20

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (D) OTHER INFORMATION: /= "88-2B-r1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CAGCAGCGTT TTGATGATTC

20

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (D) OTHER INFORMATION: /= "88C-f1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGTGTTTGCT TTAAAAGCC

19

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (D) OTHER INFORMATION: /= "88C-r3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TAAGCCTCAC AGCCCTG

17

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (D) OTHER INFORMATION: /= "CCCKR1(2)-5' Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGTAAGCTTA GAGAAGCCGG GATGGGAA

28

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iv) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: /= "CCCKR-3' Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCTCTAGAG TCAGAGACCA GCAGA

25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACAAGCTTC ACAGGGTGGA ACAAGATG

28

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTCTCTAGAC CACTTGAGTC CGTGTCA

27

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATG Met 1	GAC Asp	TAT Tyr	CAA Gln	GTG Val 5	TCA Ser	AGT Ser	CCA Pro	ACC Thr	TAT Tyr 10	GAC Asp	ATC Ile	GAT Asp	TAT Tyr 15	TAT Tyr 15	ACA Thr	48
TCG Ser	GAA Glu	CCC Pro	TGC Cys 20	CAA Gln	AAA Lys	ATC Ile	AAT Asn	GTG Val 25	AAA Lys	CAA Gln	ATC Ile	GCA Ala	GCC Ala 30	CGC Arg	CTC Leu	96
CTG Leu	CCT Pro	CCG Pro 35	CTC Leu	TAC Tyr	TCA Ser	CTG Leu	GTG Val 40	TTC Phe	ATC Ile	TTT Phe	GGT Gly	TTT Phe 45	GTG Val	GGC Gly	AAC Asn	144
ATA Ile 50	CTG Leu	GTC Val	GTC Val	CTC Leu	ATC Ile	CTG Leu 55	ATA Ile	AAC Asn	TGC Cys	AAA Lys	AGG Arg 60	CTG Leu	AAA Lys	AGC Ser	ATG Met	192
ACT Thr 65	GAC Asp	ATC Ile	TAC Tyr	CTG Leu	CTC Leu 70	AAC Asn	CTG Leu	GCC Ala	ATC Ile	TCT Ser 75	GAC Asp	CTG Leu	CTT Leu	TTC Phe	CTT Leu 80	240
CTT Leu	ACT Thr	GTC Val	CCC Pro	TTC Phe 85	TGG Trp	GCT Ala	CAC His	TAT Tyr 90	GCT Ala	GCT Ala	GCC Ala	CAG Gln	TGG Trp	GAC Asp 95	TTT Phe	288
GGA Gly	AAT Asn	ACA Thr	ATG Met 100	TGT Cys	CAA Gln	CTC Leu	TTG Leu 105	ACA Thr	GGG Gly	CTC Leu	TAT Tyr	TTT Phe 110	ATA Ile	GGC Gly	TTC Phe	336
TTC Phe	TCT Ser	GGA Gly 115	ATC Ile	TTC Phe	TTC Phe	ATC Ile 120	ATC Ile	CTC Leu	CTG Leu	ACA Thr	ATC Ile	GAT Asp 125	AGG Arg	TAC Tyr	CTG Leu	384
GCT Ala 130	ATC Ile	GTC Val	CAT His	GCT Ala	GTG Val	TTT Phe 135	GCT Ala	TTA Leu	AAA Lys	GCC Ala	AGG Arg 140	ACA Thr	GTC Val	ACC Thr	TTT Phe	432
GGG Gly 145	GTG Val	GTG Val	ACA Thr	AGT Ser	GTG Val 150	ATC Ile	ACT Thr	TGG Trp	GTG Val	GTG Val	GCT Ala	GTG Val	TTT Phe	GCC Ala	TCT Ser 160	480
CTC Leu	CCA Pro	GGA Gly	ATC Ile	ATC Ile	TTT Phe 165	ACC Thr	AGA Arg	TCT Ser	CAG Gln	AGA Arg	GAA Glu	GGT Gly	CTT Leu	CAT His 175	TAC Tyr	528
ACC Thr	TGC Cys	AGC Ser	TCT Ser	CAT His	TTT Phe 180	CCA Pro	TAC Tyr	AGT Ser 185	CAG Gln	TAT Tyr	CAA Gln	TTC Phe	TGG Trp 190	AAG Lys	AAT Asn	576
TTT Phe	CAG Gln	ACA Thr 195	TTA Leu	AAG Lys	ATG Met	GTC Val	ATC Ile 200	TTG Leu	GGG Gly	CTG Leu	GTC Val	CTG Leu	CCG Pro	CTG Leu	CTT Leu	624
GTC Val 210	ATG Met	GTC Val	ATC Ile	TGC Cys	TAC Tyr	TCG Ser 215	GGA Gly	ATC Ile	CTG Leu	AAA Lys	ACT Thr 220	CTG Leu	CTT Leu	CGG Arg	TGT Cys	672
CGA Arg 225	AAC Asn	GAG Glu	AAG Lys	AAG Lys	AGG Arg 230	CAC His	AGG Arg	GCT Ala	GTG Val	AGG Arg 235	CTT Leu	ATC Ile	TTC Phe	ACC Thr	ATC Ile 240	720
ATG Met	ATT Ile	GTT Val	TAT Tyr	TTT Phe 245	CTC Leu	TTG Leu	TGG Trp	GCT Ala	CCC Pro 250	TAC Tyr	AAC Asn	ATT Ile	GTC Val	CTT Leu 255	CTC Leu	768
CTG Leu	AAC Asn	ACC Thr	TTC Phe 260	CAG Gln	GAA Glu	TTC Phe	TTT Phe	GGC Gly 265	CTG Leu	AAT Asn	AAT Asn	TGC Cys	AGT Ser	AGC Ser	TCT Ser	816

AAC AGG TTG GAC CAA GCC ATG CAG GTG ACA GAG ACT CTT GGG ATG ACA	864
Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr	
275 280 285	
CAC TGC TGC ATC AAC CCC ATC ATC TAT GCC TTT GTC GGG GAG AAG TTC	912
His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe	
290 295 300	
AGA AAC TAC CTC TTA GTC TTC TTC CAA AAG CAC ATT GCC AAA CGC TTC	960
Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe	
305 310 315 320	
TGC AAA TGC TGT TCC ATT TTC CAG CAA GAG GCT CCC GAG CGA GCA AGT	1008
Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser	
325 330 335	
TCA GTT TAC ACC CGA TCC ACT GGG GAG CAG GAA ATA TCT GTG GGC TTG	1056
Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu	
340 345 350	
TGA	1059

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Asp Tyr Gln Val Ser Ser Pro Thr Tyr Asp Ile Asp Tyr Tyr Thr	
1 5 10 15	
Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu	
20 25 30	
Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn	
35 40 45	
Ile Leu Val Val Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met	
50 55 60	
Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu	
65 70 75 80	
Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe	
85 90 95	
Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe	
100 105 110	
Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu	
115 120 125	
Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe	
130 135 140	
Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser	
145 150 155 160	
Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Arg Glu Gly Leu His Tyr	
165 170 175	

Thr	Cys	Ser	Ser	His	Phe	Pro	Tyr	Ser	Gln	Tyr	Gln	Phe	Trp	Lys	Asn
			180					185					190		
Phe	Gln	Thr	Leu	Lys	Met	Val	Ile	Leu	Gly	Leu	Val	Leu	Pro	Leu	Leu
		195					200					205			
Val	Met	Val	Ile	Cys	Tyr	Ser	Gly	Ile	Leu	Lys	Thr	Leu	Leu	Arg	Cys
	210					215					220				
Arg	Asn	Glu	Lys	Lys	Arg	His	Arg	Ala	Val	Arg	Leu	Ile	Phe	Thr	Ile
225					230					235					240
Met	Ile	Val	Tyr	Phe	Leu	Leu	Trp	Ala	Pro	Tyr	Asn	Ile	Val	Leu	Leu
				245					250					255	
Leu	Asn	Thr	Phe	Gln	Glu	Phe	Phe	Gly	Leu	Asn	Asn	Cys	Ser	Ser	Ser
			260					265					270		
Asn	Arg	Leu	Asp	Gln	Ala	Met	Gln	Val	Thr	Glu	Thr	Leu	Gly	Met	Thr
		275					280					285			
His	Cys	Cys	Ile	Asn	Pro	Ile	Ile	Tyr	Ala	Phe	Val	Gly	Glu	Lys	Phe
	290					295					300				
Arg	Asn	Tyr	Leu	Leu	Val	Phe	Phe	Gln	Lys	His	Ile	Ala	Lys	Arg	Phe
305					310					315					320
Cys	Lys	Cys	Cys	Ser	Ile	Phe	Gln	Gln	Glu	Ala	Pro	Glu	Arg	Ala	Ser
				325					330					335	
Ser	Val	Tyr	Thr	Arg	Ser	Thr	Gly	Glu	Gln	Glu	Ile	Ser	Val	Gly	Leu
			340					345					350		